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► To cite this version:

Bienvenue Kouwaye. Regression Trees and Random forest based feature selection for malaria risk exposure prediction. 2016. hal-01336316

HAL Id: hal-01336316

<https://hal.science/hal-01336316>

Preprint submitted on 23 Jun 2016

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Regression Trees and Random forest based feature selection for malaria risk exposure prediction.

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Abstract

This paper deals with prediction of anopheles number, the main vector of malaria risk, using environmental and climate variables. The variables selection is based on an automatic machine learning method using regression trees, and random forests combined with stratified two levels cross validation. The minimum threshold of variables importance is accessed using the quadratic distance of variables importance while the optimal subset of selected variables is used to perform predictions. Finally the results revealed to be qualitatively better, at the selection, the prediction, and the CPU time point of view than those obtained by GLM-Lasso method.

Keywords : Regression trees, random forest, cross-validation, variables selection, prediction.

1 Introduction

Generally, studies about disease like chikungunya, aids, and malaria provide data set containing a high number of variables and a small number of observations. When it is important to perform prediction on the risk of these diseases, the goal is to provide a consistent heuristic to select the probable candidate predictor and perform prediction for the study and also where only explanatory data are available. Generally, experts in medicine, epidemiology, genetic, perform treatment on variables before analysis, operations of selection, and forecast. Based on their knowledge, they decide to transform some variables in classes, to fix interactions between some variables, etc. In epidemiology context, the aim of this work is to provide an automatic algorithm for variables selection based on regression trees and random forest. This procedure must overcome the treatment done by experts, generate automatically a stable, and optimal subset of

predictors, and perform prediction for an other area where the target variable is not available. There are a lot of statistical modeling approach, such as linear model (LM), linear mixed model (LMM), generalized linear (GLM), generalized linear mixed (GLMM) for selection or prediction. However, these models fail when $p > n$, the number of variables (p) is more important than the number of observations (n). Experts also assume independence among explanatory variables. A lot of methods of variables selection provide a subset for prediction but not stable, not consistent or more demanding in computation time like *Wrapper*, *embedded*, *filter*, *ranking*, and their variant [1, 2, 3]. In recent works, we proposed one method of variables selection based on combination of Lasso and GLM through a double cross-validation (LOLO-DCV) named GLM-Lasso [4, 5]. The present work combines the stratified double cross validation (LOLO-DCV), and regression trees or random forest. This implies two methods : LOLO-DCV combined with regression trees, and LOLO-DCV combined with random forest. For malaria risk prediction, four strategies of variables selection LDRT, LDCT, LDRF, and LDCF are implemented. These strategies use some criteria such as : the mean, the quadratic risk, the absolute risk of the predictions, and the CPU time of algorithm computation. Each strategy is applied on four groups of variables (original, original with village, recoded, recoded with village). Most of the algorithms implemented in our work are based on [4, 5, 6, 7, 8]. We first provided a threshold of variable importance measurement for each strategy. This threshold is very important because it puts out the importance or not of predictors. The second step is to make prediction through a double cross validation loop. The last step is to select predictors according to their frequency and make consistent prediction with the remain predictors. The results are compared to those obtained by reference method. The results obtained by such procedure are clearly better improved compared to those obtained by GLM-Lasso [4, 5] taken as the reference method. The improvement is about all properties such as the selection power, the selection accuracy, the sparsity of the best subset of variables, and the prediction. Moreover, the CPU time used to display our program is smaller than the one required by the reference method and only few climate and environmental variables are the main factors associated to the malaria risk exposure with an improved accuracy.

2 Materials

In this section, we briefly recall the description of the study area, the mosquito collection and identification as well as the data, and related variables. For more details, see [9].

2.1 Study area

The study was conducted in the district of Tori-Bossito (Republic of Benin), from July 2007 to July 2009. Tori-Bossito is on the coastal plain of Southern Benin, 40 kilometers north-east of Cotonou. This area has a subtropical climate and during the study, the rainy season lasted from May to October. Average monthly temperatures varied between 27°C and 31°C. The original equatorial forest has been cleared and the vegetation is characterized by bushes with sparse trees, a few oil palm plantations, and farms. The study area contained nine

villages (Avamé centre, Gbédjougo, Houngo, Anavié, Dohinoko, Gbétaga, Tori Cada Centre, Zébè, and Zoungoudo). Tori Bossito was recently classified as mesoendemic with a clinical malaria incidence of about 1.5 episodes per child per year [10]. Pyrethroid-resistant malaria vectors are present [11].

2.2 Mosquito collection and identification

Entomological surveys based on human landing catches (HLC) were performed in the nine villages every six weeks for two years (July 2007 to July 2009). Mosquitoes were collected at four catch houses in each village over three successive nights (four indoors and four outdoors, i.e. a total of 216 nights every six weeks in the nine villages). Five catch sites had to be changed in the course of the study (2 in Gbedjougo, 1 in Avamè, 1 in Cada, 1 in Dohinoko) and a total of 19 data collections were performed in the field from July 2007 to July 2009. In total, data from 41 catch sites are available. Each collector caught of prediccional mosquitoes landing on the lower legs and feet between 10 pm and 6 am. All mosquitoes were held in bags labeled with the time of collection. The following morning, mosquitoes were identified on the basis of morphological criteria [12, 13]. All *An. gambiae* complex and *An. funestus* mosquitoes were stored in individual tube with silica gel and preserved at 220°C. *P. falciparum* infection rates were then determined on the head and thorax of individual anopheline specimens by CSP-ELISA [14].

2.3 Environmental and behavioral data

Rainfall was recorded twice a day with a pluviometer in each village. In and around each catch site, the following information was systematically collected: (1) type of soil (dry lateritic or humid hydromorphic) assessed using a soil map of the area (map IGN Benin at 1/200 000 e , sheets NB-31-XIV and NB-31-XV, 1968) that was georeferenced and input into a GIS; (2) presence of areas where building constructions are ongoing with tools or holes representing potential breeding habitats for anopheles; (3) presence of abandoned objects (or ustensils) susceptible to be used as oviposition sites for female mosquitoes; (4) a watercourse nearby; (5) number of windows and doors; (6) type of roof (straw or metal); (7) number of inhabitants; (8) ownership of a bed-net or (9) insect repellent; And (10) normalized difference vegetation index (NDVI) which was estimated for 100 meters around the catch site with a SPOT 5 High Resolution (10 m colors) satellite image (Image Spot5, CNES, 2003, distribution SpotImage S.A) with assessment of the chlorophyll density of each pixel of the image. Due to logistical problems, rainfall measurements are only available after the second entomological survey. Consequently, we excluded the first and second survey (performed in July and August 2007 respectively) from the statistical analyses.

2.4 Variables

The dependent variable was the number of Anopheles collected in a house over the three nights of each catch and the explanatory variables were the environmental factors, i.e. the mean rainfall between two catches (classified according to quartile), the number of rainy days in the ten days before the catch (3 classes [0], [24], >4 days), the season during which the catch was carried out (4 classes:

end of the dry season from February to April; beginning of the rainy season from May to July; end of the rainy season from August to October; beginning of the dry season from November to January), the type of soil 100 meters around the house (dry or humid), the presence of constructions within 100 meters of the house (yes/no), the presence of abandoned tools within 100 meters of the house (yes/no), the presence of a watercourse within 500 meters of the house (yes/no), NDVI 100 meters around the house (classified according to quartile), the type of roof (straw or Sheet metal), the number of windows (classified according to quartile), the ownership of bed nets (yes/no), the use of insect repellent (yes/no), and the number of inhabitants in the house (classified according to quartile). These pre-treatments based on the knowledge of experts in entomology, and medicine operated on some original variables generate a second type of variables called recoded variables. The original and recoded variables are described in Table 4. Two types of variables set are used : the first set, the original variables with all variables obtained by interactions; The second set, the recoded variables with all variables obtained by interactions. For knowing the effect of the village on the selection method and prediction, four groups of variables are considered : Group 1 (original variables), Group 2 (original variables with village as fixed effect), Group 3 (recoded variables), and Group 4 (recoded variables with village as fixed effect)

3 Methodology

3.1 Variables importance

For individual tree, the variable importance is defined used the out-of-bag sampling like :

$$VI^T(X^p) = (\widetilde{errOOB}_t^p - errOOB_t) \quad (1)$$

The naive importance measure in tree-based ensemble methods is to merely count the number of times each variable is selected by all individual tree in the group of trees. There also exist the "Gini importance" measurement used in random forest for classification. The more advanced variable importance measurement in random forest is the "permutation accuracy importance" defined as:

$$VI^{RF}(X^p) = \frac{1}{ntree} \sum_{t=1}^{ntree} (\widetilde{errOOB}_t^p - errOOB_t) \quad (2)$$

where VI^T is variable importance of a tree, VI^{RF} is variable importance of a random forest, X^p is the p -th variable, OOB_t the out-of-bag of tree t , \widetilde{OOB}_t^p the sample obtained by randomly permuting the value of X^p in OOB_t and $errOOB_t$ the out-of-bag error for the tree t , $ntree$ the number of regression trees in the random forest.

The Gini importance, and the permutation accuracy importance measures are employed as variable selection criteria in many recent study in various disciplines. The effects induced by the differences in scale level of the predictors are more pronounced for the **randomForest** function, where variable selection in the individual tree is biased, than the one with **cforest** function where the individual trees are unbiased [15, 16]. It has been also shown that if **cforest** function is used with bootstrap sampling, the variables selection frequencies of

the categorical predictors still depend on their number of categories. Variable importance has a sensitivity to the number of observations and the number of variables. This sensitivity is reduced with increasing number of true variables. Variable importance has also sensitivity to $mtry$ the minimum number of observations at a node for splitting, and $ntree$ the maximal number of trees in forest. It has been shown that for a fixed number of observations and variables, the effect of taking a larger value for $mtry$ is evident. Indeed, the magnitude of variable importance is more double starting from $mtry = 14$ to $mtry = 100$, and it again increases with $mtry = 200$. The effect of $ntree$ is less visible but taking $ntree = 2000$ leads to better stability [17]. A lot of strategies have been developed for variable selection. The recursive elimination of feature based on variable importance developed by Avlarez de André runs like this. They first compute random forest variable importance. Then, at each step they eliminate the 20% of variables having the less importance and build a new forest with the remaining variables. They finally select the set of variables leading to the smallest *OOB* error rate of a forest defined by

$$errOOB = \frac{1}{n} Card\{i \in \{1, \dots, n\} | y_i \neq \hat{y}_i\} \quad (3)$$

where \hat{y}_i is the most frequent label predict by trees t for which (x_i, y_i) is in the OOB_t sample [3]. But this proposition of variables elimination is arbitrary, and the method does not depend on the data.

Robin Genuer proposed an other method of variable selection based on variable importance stratified in two steps [17]. The step 1 is a preliminary ranking which consisting in sorting the variables in decreasing order of Random forest scores of importance, and canceling the variables of small importance, m is the number of remaining at the second step, he selected the variables involved in the model leading to the smallest *OOB* error and at the end constructed an ascending sequence of Random forest models by invoking, and testing the variables stepwise. The variables of the last model are selected. But this method lacks of precision because in the step 1 this strategy is sensible when it exist irrelevant variables, and at last step, variables invoking or testing can be sensitive to high correlation among variables. The method to access variable importance proposed by Daz-Uriarte [18] in scaled, unscaled, and Gini version is only available when the dependent variable is a factor.

3.2 Performance and accuracy in variables selection for strategies

This part of the work is based on simulated data. It is necessary to show the power of each strategy to reduce effectively the number of variables and select the right variables in the optimal subset for prediction. Let \mathbf{V}^R and \mathbf{V}^W the set of the real, and wrong variables respectively, \mathbf{S}^R , \mathbf{S}^W the set of the real, and wrong selected variables respectively. Let $\mathbf{V} = \mathbf{V}^R \cup \mathbf{V}^W$ and $\mathbf{S} = \mathbf{S}^R \cup \mathbf{S}^W$.

3.2.1 Selection power

It is defined as the ratio of the number of variables selected on the number of total variables (real and wrong). This quantity gives an idea of percentage of

elimination of variables. The selection power is noted SP and defined as :

$$SP = \frac{Card(\mathbf{S})}{Card(\mathbf{V})} \quad (4)$$

3.2.2 Selection accuracy

It is defined as the ratio of the number of real variables selected on the number of total variables selected. This quantity gives the accuracy selection of variables. It is noted SA and defined as :

$$SA = \frac{Card(\mathbf{S}^R)}{Card(\mathbf{S})} \quad (5)$$

3.3 Strategy parameters construction

The parameters used in the strategies for variables selection are, the minimum threshold of variables importance, the minimum number of observations at each node before splitting in trees, and the maximum number of trees in forest building.

3.3.1 Heuristic of variable importance measurement

The strategy of variable importance measurement proposed in this paper is based on a minimum threshold. For any model of regression trees and random forest, if any variable has importance greater than this threshold, it is considered as important variable in the model. One of the difficulties in this study is the decision of the minimum of importance of variable. We have a lot of techniques to check this number. The strategy proposed by Genuer et al [17] is sensible when it exist irrelevant variables. A classical alternative is to select the threshold according to some elbow finding strategy on the variable importance mean curve. In this paper we propose a new strategy running like this : we run the full model using the whole data frame n_r times (default $n_r = 100$) with the default parameters. The matrix of variables important noted M_{VI} is a $n_r \times q$ -matrix defined as :

$$M_{VI} = \begin{pmatrix} VI_{11} & VI_{12} & \dots & VI_{1n_r} \\ VI_{21} & VI_{22} & \dots & VI_{2n_r} \\ \vdots & \vdots & & \vdots \\ VI_{q1} & VI_{q2} & \dots & VI_{qn_r} \end{pmatrix}$$

VI_{ij} is the importance of i^{th} variable at j^{th} repetition, $1 \leq i \leq q$ and $1 \leq j \leq n_r$. Let

$$M_{VI} = (VI_{.1}, VI_{.2}, \dots, VI_{.n_r})$$

if

$$VI_{.i} = (VI_{1i}, VI_{2i}, \dots, VI_{qi})^t$$

then

$$\sigma_i = \min\{VI_{.i}, VI_{.i} \neq \theta, 1 \leq i \leq n_r\}$$

and

$$\sigma = (\sigma_1, \sigma_2, \dots, \sigma_{n_r})$$

where A^t is the transposed of the matrix A , and θ is the null vector. The minimum threshold of variables importance noted VI_{min} is defined as :

$$VI_{min} = \min(\sigma) + sd(\sigma) \quad (6)$$

3.3.2 Parameters *mtry* and *ntree* accessing

These parameters are accessed through a simple cross validation process. The data set is divided into two parts : E_A the learning set, and E_T the test set. On E_A , it has been performed one kind of variable selection method varying one specific parameter. For the regression tree, the parameter concerned *mtry*, the minimum number of observations that must exist at a node in order for a split to be attempted. For the forest, this parameter is *ntree*, the maximal number of trees in the forest. These parameters will be noted m for simplification of notations, $1 \leq m \leq n_{obs}$ where n_{obs} is the number of observations in E_A . For each value of m , the corresponding regression tree or the random forest provides a vector of importance $VI_{\cdot, m}$. Let \widehat{VI}_m the vector of mean of the vectors $VI_{\cdot, m}$. The quadratic distance is defined as :

$$d(\widehat{VI}_m, VI_{\cdot, m}) = \left[\sum_{j=1}^{n_{var}} (\widehat{VI}_m - VI_{j, m})^2 \right]^{1/2}, \quad 1 \leq m \leq n_{obs} \quad (7)$$

where n_{var} is the number of variables

The parameter m is determined by optimizing the quadratic distance of importance. Let define :

$$\mathcal{H} = \underset{m}{\text{Arg min}} d(\widehat{VI}_m, VI_{\cdot, m}) \quad (8)$$

If $\text{Card}(\mathcal{H}) = 1$ then $\mathcal{H} = \{h_0\}$ and

$$mtry = ntree = h_0 \quad (9)$$

If $\text{Card}(\mathcal{H}) \geq 2$ then

$$mtry = \min\{\mathcal{H}\} \text{ and } ntree = \max\{\mathcal{H}\} \quad (10)$$

A regression tree with this value of *mtry* or a Random forest (RF) with this value of *ntree* will perform prediction on E_T . All this process will be repeated until prediction is computed for all observations.

3.3.3 Algorithm of variables selection and prediction

This algorithm is similar to the one developed in a recent work [5, 4].

3.4 Variables selection strategies

Four strategies of variables selection are implemented and compared to the reference method GLM-Lasso developped in [5, 4]. The first strategy, LDRT is a combination of LOLO-DCV (Leave-one-out-double-cross-validation), and regression tree (RT) [19, 20]; The second LDCT is a combination of LOLO-DCV and conditional tree (CT) [21]; The third LDRF, a combination of LOLO-DCV

Algorithm 3.1 LOLO-DCV-Tree-Forest

1. Determination of VI_{min}
 2. The data are separated in N -folds
 3. At each step of the first level
 - (a) The folds are regrouped in two parts : E_A and E_T , E_A : the learning set which contained the observations of $(N - 1)$ -folds, E_T : the test set, contained the observations of the last fold.
 - (b) Holding-out E_T
 - (c) The second level of cross-validation
 - i. A full cross validation is computed on E_A for determination of the first model construction parameter m (*mtry* or *ntree*).
 - ii. Tree or forest model \mathcal{M}_m is computed on E_A using m
 - iii. The importance of variables $VI_{\cdot m}$ is accessed.
 - iv. Predictions are performed using a \mathcal{M}_m model on E_T
 4. The step (3c) is repeated until predictions are performed for all observations, and a matrix \mathbf{M}_{VI} of importance is recorded.
 5. The vector mean \widehat{VI} (representative) of \mathbf{M}_{VI} is determined.
 6. The selection of each variable is done by \widehat{VI} using VI_{min} .
-

and Random forest (RF) [16, 22, 23]; And the last LDCF is a combination of LOLO-DCV and conditional forest (CF) [21]. The selection power, the selection accuracy of each strategy is determined on simulated data. The model construction parameter for each strategy is accessed based on the quadratic distance between importance and the mean of importance. Each strategy based on the threshold of the minimum of variable importance selects an optimal subset of variables.

4 Results

First of all, we show the numerical convergence of VI_{min} in Equation (6) for each strategy on simulated data. The results are shown in table 1 and figure 2. We also show the power of each strategy to reduce the number of variables, and select the true variables in the optimal subset for prediction. The results are presented in table 1

4.1 Simulated study

We simulated a data base of n observations and p true variables. We generated p -explanatory variables X , and the target variable Y knowing that $(Y|X) \sim \mathcal{P}(\mathbb{E}(X\beta))$ where β is the vector of coefficients of X , and $\mathcal{P}(\mathbb{E}(X\beta))$ is a Poisson distribution of parameter $\mathbb{E}(X\beta)$. We also generated another p -variables Z which don't participate to the determination of Y . One of the strength of the algorithm is its capacity to avoid in selection the wrong variables at most possible. The final number of variable in learning is $2 \times p$ the set X of generic explanatory variables contains : Gaussian variable, $X_N^p \sim \mathcal{N}(\mu_p, \sigma_p^2)$; discrete variable which values are in range $(1, 10)$, categorical variables with at most 10 modalities, and variables following Poisson distribution of parameter λ_{X_p} . For illustration, $\beta \sim \mathcal{N}(0, 1)$, $\mu_p \in \{-1, 0, 1\}$, $\sigma_p = 1$, and $\lambda_{X_p} = 1$

4.2 Application to malaria data

The results of application of strategies LDRT, LDCT, LDRF, and LDCF on malaria data are shown in tables 2, and 3. The strategy LDRT do not converge. The threshold of variable importance is null for LDCF. So any variable with non null importance will be importante. The threshold of variable importance is very high for LDCT, table 2. The strategies LDCT, LDCF, and LDRF have a mean in prediction which is equal to the mean of observations. LDRF has the low quadratic risk, absolute risk, the low computation time, and the most sparse subset of remained variables but its mean in prediction is greater than the one of observations, table 3.

5 Discussion

The table 1 shows that computation is not compiled for LDRT if the number of variables is greater than 40 approximatively. This is due to the non convergence of the **rpart** function in the package **rpart** for construction of regression tree. For Random forest, the convergence of the percentage of selected variables is not ensured. But the convergence is obtained when we combined LOLO-DCV

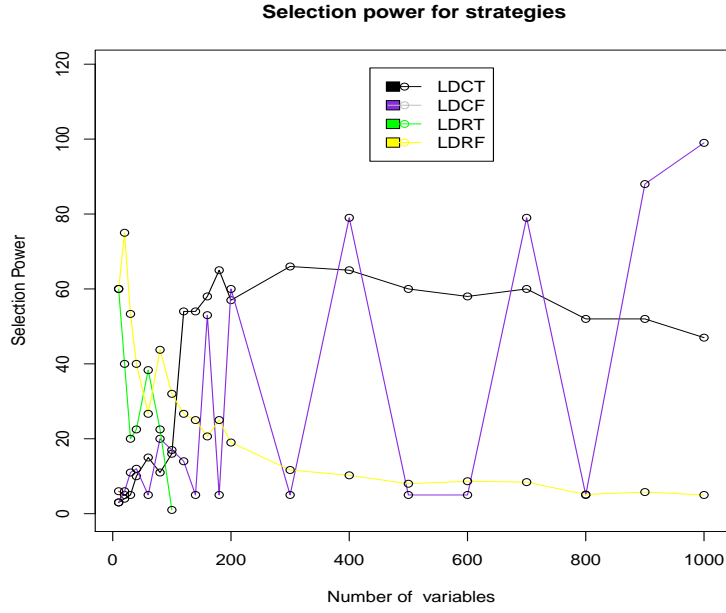


Figure 1: **Selection power of strategies according to number of variables.** Each line shows the trajectory of the selection for each strategy on simulated data.

Table 1: **Summary on results of selection power and selection accuracy for different strategies.** MVI= Minimum variable importance, SP= selection power, SA= Selection accuracy

number of variables		250	300	350	400	500	80	600	800
LDRT	SP	-	-	-	-	-	-	-	-
	SA	-	-	-	-	-	-	-	-
	MVI	-	-	-	-	-	-	-	-
LDCT	SP	38.00	45	46	47.00	38.0	44.0	46.00	36.00
	SA	26.88	26.11	26.5	15.33	9.75	9	6.83	5.71
	MVI	2.00	2	2.20	2.2	2.0	2.00	2.00	2
LDRF	SP	20.62	21.67	17.00	15.00	11.75	9.00	9.33	8.57
	SA	38.12	33.33	33	23	14.75	12	8.83	7.14
	MVI	1.00	1.0	1	1.00	1	1.00	1.00	1.0
LDCF	SP	48	62.00	5.0	67.00	88	5	5.00	5.00
	SA	30	34.44	2.5	22.33	22	1	0.83	0.71
	MVI	0	0	0	0	0	0	0	0

with Random Forest (LDRF). The percentage of remained variables is around 5%. The results are also shown in figure 1. It is evident that the convergence

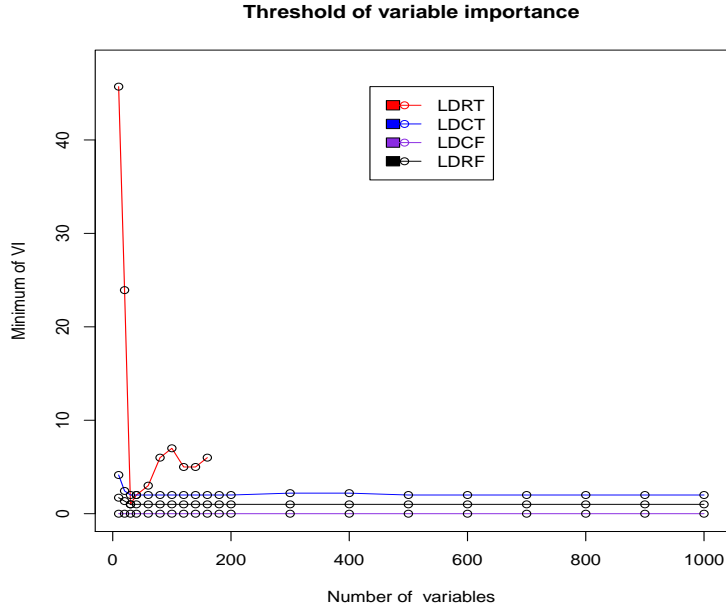


Figure 2: **Threshold of variable importance measurement.** Each line shows the trajectory of the variable importance for each strategy on simulated data.

Table 2: **Threshold of variable importance measurement on real data.**

	LDRT	LDCT	LDRF	LDCF
VI_{min}	-	5.12507	1.1	0

Table 3: **Summary on results of selection power, selection accuracy, and minimum of variable importance on malaria data**

Method	Mean	QR	Absolute risk	Remain variables	Time CPU
Observations	3.74	-	-	-	-
GLM-Lasso	3.74	54.54	3.669	3	25786.87
LDRT	-	-	-	-	-
LDCT	3.74	50.56	3.217	4	24378.38
LDRF	3.75	49.56	2.876	3	6715.09
LDCF	3.74	49.987	3.001	4	24830.34

of LDCF is not stable because the alternative high and low percentage of remained variables. The figure 2 confirms the non convergence of LDRT over

approximatively 40 variables. Even if the algorithm did not converge for all number of variable, the minimum is attempted, and the trajectory is convex. For the strategies LDCT, LDRF, and LDCF, the minimum of variable importance converges, and the results are shown in the line "MVI" of table 1, and in figure 2 for each strategy. This denotes that the algorithm can compute correctly the threshold of importance of variable for any number of variable but not for LDRT. The results of application about malaria data are shown in table 3. The minimum of variable importance that we got for each method are noted in table 2. Unfortunately this minimum for LDCF is null. It means that for any positive value, the variable is important but four variable are selected at the end. For LDCT, the threshold of importance is very high, table 2 nevertheless four variables are remained in the final model, table 3. It denotes that only few variables are important in the model. The methods which have the mean in prediction equals to the mean of observations are LDCT, and LDCF. LDCF is the best in selection accuracy. LDRF has the lowest quadratic risk, the lower absolute risk but it isn't the best prediction. LDRF is the most sparse method with three variables. Unlike LDRF, LDCF, and LDCT which are more time consuming table 3.

6 Conclusion

In this work, we implemented an algorithm for the prediction of malaria risk using environmental and climate variables. We performed the variables selection using an automatic machine learning by a method combining regression trees or random forest, and stratified two levels cross validation. The minimum threshold of variable importance is computed. variables selected by each strategy are used to perform prediction. The results obtained with this method is clearly improved by those obtained with the combination of Lasso, and LOLO-DCV (GLM-Lasso) taken as reference method. The improvement concerned all properties such as the quality of the selection, and prediction. Moreover, this method didn't need interaction between variables, the pre-treatments of experts were overcome, and the CPU time used to display our program is smaller than the one required by the reference method. The optimal subset of variables for prediction contained season, mean rain fall, and vegetation index.

7 Appendix

Table of variables Description The authors have declared that no competing interests exist.

Table 4: **Description of variables.** Variables with star are recoded.

	Nature	Number of modalities	Modalities
Repellent	Non-numeric	2	Yes/ No
Bed-net	Non-numeric	2	Yes/ No
Type of roof	Non-numeric	2	Sheet metal/ Straw
Utensils	Non-numeric	2	Yes/ No
Presence of constructions	Non-numeric	2	Yes/ No
Type of soil	Non-numeric	2	Humid/ Dry
Water course	Non-numeric	2	Yes/ No
Majority class *	Non-numeric	3	1/2/3
Season	Non-numeric	4	1/2/3/4
Village*	Non-numeric	9	
House *	Non-numeric	41	
Rainy days before mission *	Non-numeric	3	Quartile
Rainy days during mission	Numeric	Discrete	0/1/.../3
Fragmentation index *	Non-numeric	4	Quartile
Openings*	Non-numeric	4	Quartile
Nber of inhabitants *	Non-numeric	3	Quartile
Mean rainfall *	Non-numeric	4	Quartile
Vegetation*	Non-numeric	4	Quartile
Total Mosquitoes	Numeric	Discrete	0/.../481
Total Anopheles	Numeric	Discrete	0/.../87
Anopheles infected	Numeric	Discrete	0/.../9

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